RAW SEQUENCE LISTING   DATE: 08/23/2004
PATENT APPLICATION: US/09/754,014A   TIME: 16:08:38

Input Set : A:\09-754,014.txt
Output Set: N:\CRF4\08232004\I754014A.raw

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 3 <110> APPLICANT: Valentis, Inc.
 4         Nordstrom, Jeff
 5         Freimark, Bruce
 6         Deshpande, Deepa
 8 <120> TITLE OF INVENTION: Gene Expression and Delivery Systems and Uses
10 <130> FILE REFERENCE: 213-0063US
12 <140> CURRENT APPLICATION NUMBER: US 09/754,014A
13 <141> CURRENT FILING DATE: 2001-01-03
15 <150> PRIOR APPLICATION NUMBER: US 08/948,958
16 <151> PRIOR FILING DATE: 1997-10-10
18 <150> PRIOR APPLICATION NUMBER: US 60/028,687
19 <151> PRIOR FILING DATE: 1996-10-10
21 <160> NUMBER OF SEQ ID NOS: 19
23 <170> SOFTWARE: PatentIn version 3.3
25 <210> SEQ ID NO: 1
26 <211> LENGTH: 328
27 <212> TYPE: PRT
28 <213> ORGANISM: Homo sapiens
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36 Ala Ser Pro Leu Val Ala Ile Trp Glu Leu Lys Lys Asp Val Tyr Val
37             20                  25                  30
40 Val Glu Leu Asp Trp Tyr Pro Asp Ala Pro Gly Glu Met Val Val Leu
41         35                  40                  45
44 Thr Cys Asp Thr Pro Glu Glu Asp Gly Ile Thr Trp Thr Leu Asp Gln
45     50                  55                  60
48 Ser Ser Glu Val Leu Gly Ser Gly Lys Thr Leu Thr Ile Gln Val Lys
49 65                  70                  75                  80
52 Glu Phe Gly Asp Ala Gly Gln Tyr Thr Cys His Lys Gly Gly Glu Val
53             85                  90                  95
56 Leu Ser His Ser Leu Leu Leu Leu His Lys Lys Glu Asp Gly Ile Trp
57             100                 105                 110
60 Ser Thr Asp Ile Leu Lys Asp Gln Lys Glu Pro Lys Asn Lys Thr Phe
61         115                 120                 125
64 Leu Arg Cys Glu Ala Lys Asn Tyr Ser Gly Arg Phe Thr Cys Trp Trp
65     130                 135                 140
68 Leu Thr Thr Ile Ser Thr Asp Leu Thr Phe Ser Val Lys Ser Ser Arg
69 145                 150                 155                 160
72 Gly Ser Ser Asp Pro Gln Gly Val Thr Cys Gly Ala Ala Thr Leu Ser
73             165                 170                 175
76 Ala Glu Arg Val Arg Gly Asp Asn Lys Glu Tyr Glu Tyr Ser Val Glu
77             180                 185                 190
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Input Set : A:\09-754,014.txt
Output Set: N:\CRF4\08232004\I754014A.raw

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80  Cys Gln Glu Asp Ser Ala Cys Pro Ala Ala Glu Glu Ser Leu Pro Ile
81          195             200             205
84  Glu Val Met Val Asp Ala Val His Lys Leu Lys Tyr Glu Asn Tyr Thr
85      210             215             220
88  Ser Ser Phe Phe Ile Arg Asp Ile Ile Lys Pro Asp Pro Pro Lys Asn
89  225             230             235             240
92  Leu Gln Leu Lys Pro Leu Lys Asn Ser Arg Gln Val Glu Val Ser Trp
93              245             250             255
96  Glu Tyr Pro Asp Thr Trp Ser Thr Pro His Ser Tyr Phe Ser Leu Thr
97          260             265             270
100 Phe Cys Val Gln Val Gln Gly Lys Ser Lys Arg Glu Lys Lys Asp Arg
101         275             280             285
104 Val Phe Thr Asp Lys Thr Ser Ala Thr Val Ile Cys Arg Lys Asn Ala
105     290             295             300
108 Ser Ile Ser Val Arg Ala Gln Asp Arg Tyr Tyr Ser Ser Ser Trp Ser
109 305             310             315             320
112 Glu Trp Ala Ser Val Pro Cys Ser
113             325
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117 <211> LENGTH: 987
118 <212> TYPE: DNA
119 <213> ORGANISM: homo sapiens
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124 gtggccatat gggaactgaa gaaagatgtt tatgtcgtag aattggattg gtatccggat  120
126 gcccctggag aaatggtggt cctcacctgt gacacccctg aagaagatgg tatcacctgg  180
128 accttggacc agagcagtga ggtcttaggc tctggcaaaa ccctgaccat ccaagtcaaa  240
130 gagtttggag atgctggcca gtacacctgt cacaaaggag gcgaggttct aagccattcg  300
132 ctcctgctgc ttcacaaaaa ggaagatgga atttggtcca ctgatatttt aaaggaccag  360
134 aaagaaccca aaaataagac ctttctaaga tgcgaggcca agaattattc tggacgtttc  420
136 acctgctggt ggctgacgac aatcagtact gatttgacat tcagtgtcaa aagcagcaga  480
138 ggctcttctg accccaagg ggtgacgtgc ggagctgcta cactctctgc agagagagtc   540
140 agagggaca acaaggagta tgagtactca gtggagtgcc aggaggacag tgcctgccca   600
142 gctgctgagg agagtctgcc cattgaggtc atggtggatg ccgttcacaa gctcaagtat  660
144 gaaaactaca ccagcagctt cttcatcagg gacatcatca acctgacccc acccaagaac  720
146 ttgcagctga agccattaaa gaattctcgg caggtggagg tcagctggga gtaccctgac  780
148 acctggagta ctccacattc ctacttctcc ctgacattct gcgttcaggt ccagggcaag  840
150 agcaagagag aaaagaaaga tagagtcttc acggacaaga cctcagccac ggtcatctgc  900
152 cgcaaaaatg ccagcattag cgtgcgggcc caggaccgct actatagctc atcttggagc  960
154 gaatgggcat ctgtgccctg cagttag                                      987
157 <210> SEQ ID NO: 3
158 <211> LENGTH: 987
159 <212> TYPE: DNA
160 <213> ORGANISM: artificial sequence
162 <220> FEATURE:
163 <223> OTHER INFORMATION: codon optimized Human IL-12 p40
165 <400> SEQUENCE: 3
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168 gtggccatct gggagctgaa gaaggacgtg tacgtggtgg agctggactg gtaccccgac  120
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RAW SEQUENCE LISTING   DATE: 08/23/2004
PATENT APPLICATION: US/09/754,014A   TIME: 16:08:38

Input Set : A:\09-754,014.txt
Output Set: N:\CRF4\08232004\I754014A.raw

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170 gcccccggcg agatggtggt gctgacctgc gacacccccg aggaggacgg catcacctgg    180
172 accctggacc agagcagcga ggtgctgggc agcggcaaga ccctgaccat ccaggtgaag    240
174 gagttcggcg acgccggcca gtacacctgc cacaagggcg gcgaggtgct gagccacagc    300
176 ctgctgctgc tgcacaagaa ggaggacggc atctggagca ccgacatcct gaaggaccag    360
178 aaggagccca agaacaagac cttcctgcgc tgcgaggcca agaactacag cggccgcttc    420
180 acctgctggt ggctgaccac catcagcacc gacctgacct tcagcgtgaa gagcagcagg    480
182 ggcagcagcg acccccaggg cgtgacctgc ggcgccgcca ccctgagcgc cgagcgcgtg    540
184 cgcggcgaca acaaggagta cgagtacagc gtggagtgcc aggaggacag cgcctgcccc    600
186 gccgccgagg agagcctgcc catcgaggtg atggtggacg ccgtccacaa gctgaagtac    660
188 gagaactaca ccagcagctt cttcatccgc gacatcatca gcccgaccc ccccaagaac    720
190 ctgcagctga gccccctgaa gaacagccgc caggtggagg tgagctggga gtaccccgac    780
192 acctggagca ccccccacag ctacttcagc ctgaccttct gcgtgcaggt gcagggcaag    840
194 agcaagcgcg agaagaagga ccgcgtgttc accgacaaga ccagcgccac cgtgatctgc    900
196 cgcaagaacg ccagcatcag cgtgcgcgcc caggaccgct actacagcag cagctggagc    960
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202 <211> LENGTH: 987
203 <212> TYPE: DNA
204 <213> ORGANISM: artificial sequence
206 <220> FEATURE:
207 <223> OTHER INFORMATION: codon optimized human IL-12 p40
209 <400> SEQUENCE: 4
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212 gtggccatct gggagctgaa gaaagacgtg tacgtggtcg agctggactg gtaccccgac    120
214 gccccgggcg agatggtggt cctgacctgc gacaccccccg aggaagacgg catcacctgg    180
216 accctggacc agagcagtga ggtgctgggc tccggcaaga ccctgaccat ccaggtgaag    240
218 gagttcggcg acgccggcca gtacacctgc cacaagggag gcgaggtgct gagccactcc    300
220 ctcctgctgc tccacaaaaa ggaggacggc atctggagca ccgacatcct gaaggaccag    360
222 aaggagccca agaacaagac cttcctgcgc tgcgaggcca agaactacag cggccgcttc    420
224 acctgctggt ggctgaccac gatcagcacc gacctgacct tcagtgtgaa gagcagcagg    480
226 ggctccagcg acccccaggg cgtgacctgc ggcgctgcca ccctgagcgc cgagcgcgtg    540
228 cgcggcgaca acaaggagta cgagtacagc gtggagtgcc aggaagactc cgcctgcccc    600
230 gccgctgagg agagcctgcc catcgaggtg atggtggacg ccgttcacaa gctgaagtac    660
232 gagaactaca ccagcagctt cttcatccgc gacatcatca gcctgacccc acccaagaac    720
234 ctccagctga gcccctcaa gaactcccgc caggtggagg tgagctggga gtaccccgac    780
236 acctggagca cgccccactc ctacttctcc ctgaccttct gcgtgcaggt ccagggcaag    840
238 agcaagcgcg agaagaaaga ccgggtgttc accgacaaga ccagcgccac cgtcatctgc    900
240 cgcaagaacg ccagcatcag cgtgcgcgcc caggaccgct actatagctc ctcttggagc    960
242 gagtgggcca gcgtgccctg ctcctag                                        987
245 <210> SEQ ID NO: 5
246 <211> LENGTH: 219
247 <212> TYPE: PRT
248 <213> ORGANISM: homo sapiens
250 <400> SEQUENCE: 5
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253 1               5                   10                  15
256 Asp His Leu Ser Leu Ala Arg Asn Leu Pro Val Ala Thr Pro Asp Pro
257             20                  25                  30
260 Gly Met Phe Pro Cys Leu His His Ser Gln Asn Leu Leu Arg Ala Val
```

```
261          35                    40                    45
264 Ser Asn Met Leu Gln Lys Ala Arg Gln Thr Leu Glu Phe Tyr Pro Cys
265      50                    55                    60
268 Thr Ser Glu Glu Ile Asp His Glu Asp Ile Thr Lys Asp Lys Thr Ser
269 65                    70                    75                    80
272 Thr Val Glu Ala Cys Leu Pro Leu Glu Leu Thr Lys Asn Glu Ser Cys
273                 85                    90                    95
276 Leu Asn Ser Arg Glu Thr Ser Phe Ile Thr Asn Gly Ser Cys Leu Ala
277             100                   105                   110
280 Ser Arg Lys Thr Ser Phe Met Met Ala Leu Cys Leu Ser Ser Ile Tyr
281         115                   120                   125
284 Glu Asp Leu Lys Met Tyr Gln Val Glu Phe Lys Thr Met Asn Ala Lys
285     130                   135                   140
288 Leu Leu Met Asp Pro Lys Arg Gln Ile Phe Leu Asp Gln Asn Met Leu
289 145                   150                   155                   160
292 Ala Val Ile Asp Glu Leu Met Gln Ala Leu Asn Phe Asn Ser Glu Thr
293             165                   170                   175
296 Val Pro Gln Lys Ser Ser Leu Glu Glu Pro Asp Phe Tyr Lys Thr Lys
297         180                   185                   190
300 Ile Lys Leu Cys Ile Leu Leu His Ala Phe Arg Ile Arg Ala Val Thr
301     195                   200                   205
304 Ile Asp Arg Val Thr Ser Tyr Leu Asn Ala Ser
305     210                   215
308 <210> SEQ ID NO: 6
309 <211> LENGTH: 660
310 <212> TYPE: DNA
311 <213> ORGANISM: homo sapiens
313 <400> SEQUENCE: 6
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316 ttggccagaa acctccccgt ggccactcca gacccaggaa tgttcccatg ccttcaccac    120
318 tcccaaaacc tgctgagggc cgtcagcaac atgctccaga aggccagaca aactctagaa    180
320 ttttacccct gcacttctga agagattgat catgaagata tcacaaaaga taaaaccagc    240
322 acagtggagg cctgtttacc attggaatta accaagaatg agagttgcct aaattccaga    300
324 gagacctctt tcataactaa tgggagttgc ctggcctcca gaaagacctc ttttatgatg    360
326 gccctgtgcc ttagtagtat ttatgaagac ttgaagatgt accaggtgga gttcaagacc    420
328 atgaatgcaa agcttctgat ggatcctaag aggcagatct ttctagatca aaacatgctg    480
330 gcagttattg atgagctgat gcaggccctg aatttcaaca gtgagactgt gccacaaaaa    540
332 tcctcccttg aagaaccgga tttttataaa actaaaatca agctctgcat acttcttcat    600
334 gctttcagaa ttcgggcagt gactattgac agagtgacga gctatctgaa tgcttcctaa    660
337 <210> SEQ ID NO: 7
338 <211> LENGTH: 660
339 <212> TYPE: DNA
340 <213> ORGANISM: artificial sequence
342 <220> FEATURE:
343 <223> OTHER INFORMATION: Codon optimized Human IL-12 p35
345 <400> SEQUENCE: 7
346 atgtgccccg cccgcagcct gctgctggtg gccaccctgg tgctgctgga ccacctgagc     60
348 ctggcccgca acctgcccgt ggccaccccc gaccccggca tgttcccctg cctgcaccac    120
350 agccagaacc tgctggcggc cgtgagcaac atgctgcaga aggccgcgca gaccctggag    180
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352 ttctacccct gcaccagcga ggagatcgac cacgaggaca tcaccaagga caagaccagc    240
354 accgtggagg cctgcctgcc cctggagctg accaagaacg agagctgcct gaacagccgc    300
356 gagaccagct tcatcaccaa cggcagctgc ctggccagcc gcaagaccag cttcatgatg    360
358 gccctgtgcc tgagcagcat ctacgaggac ctgaagatgt accaggtgga gttcaagacc    420
360 atgaacgcca agctgctgat ggaccccaag ctccagatct tcctggacca gaacatgctg    480
362 gccgtgatcg acgagctgat gcaggccctg aacttcaaca gcgagaccgt gccccagaag    540
364 agcagcctgg aggagcccga cttctacaag accaagatca agctgtgcat cctgctgcac    600
366 gccttccgca tccgcgccgt gaccatcgac cgcgtgacca gctacctgaa cgccacctga    660
369 <210> SEQ ID NO: 8
370 <211> LENGTH: 660
371 <212> TYPE: DNA
372 <213> ORGANISM: artificial sequence
374 <220> FEATURE:
375 <223> OTHER INFORMATION: codon optimized Human IL-12 p35

377 <400> SEQUENCE: 8
378 atgtgccccg cccgcagcct gctgctcgtg gccaccctgg tgctcctgga ccacctcagc     60
380 ctggcccgca acctccccgt ggccacccca gaccccggca tgttcccatg cctgcaccac    120
382 agccagaacc tgctggcggc cgtgagcaac atgctgcaga aggccgcgca gaccctggag    180
384 ttctacccct gcaccagcga ggagatcgac cacgaggaca tcaccaagga caagaccagc    240
386 accgtggagg cctgcctgcc cctcgagtta accaagaacg agagctgcct caacagccgc    300
388 gagacctcct tcatcaccaa cggcacttgc ctggcctccc gcaagaccag cttcatgatg    360
390 gccctgtgcc tgagctccat ctacgaggac ctgaagatgt accaggtgga gttcaagacc    420
392 atgaacgcca agctcctgat ggaccccaag ctccagatct tcctggacca gaacatgctg    480
394 gccgtgatcg acgagctgat gcaggccctg aacttcaaca gcgagaccgt gccccagaag    540
396 agcagcctgg aggagcccga cttctacaag accaagatca agctgtgcat cctgctgcac    600
398 gccttccgca tccgggccgt gaccatcgac cgcgtgacca gctacctgaa cgccacgtga    660
401 <210> SEQ ID NO: 9
402 <211> LENGTH: 58
403 <212> TYPE: DNA
404 <213> ORGANISM: artificial sequence
406 <220> FEATURE:
407 <223> OTHER INFORMATION: synthetic 5' UTR

409 <400> SEQUENCE: 9
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413 <210> SEQ ID NO: 10
414 <211> LENGTH: 45
415 <212> TYPE: DNA
416 <213> ORGANISM: artificial sequence
418 <220> FEATURE:
419 <223> OTHER INFORMATION: synthetic intron where tract of random nucleotides not shown
422 <220> FEATURE:
423 <221> NAME/KEY: misc_feature
424 <222> LOCATION: (1)..(9)
425 <223> OTHER INFORMATION: 5' splice site, where actual splice between nucleotide 3 and
427 <220> FEATURE:
428 <221> NAME/KEY: misc_feature
429 <222> LOCATION: (10)..(15)
430 <223> OTHER INFORMATION: optional restriction enzyme site
432 <220> FEATURE:
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4

RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 08/23/2004
PATENT APPLICATION: US/09/754,014A   TIME: 16:08:39

Input Set : **A:\09-754,014.txt**
Output Set: **N:\CRF4\08232004\I754014A.raw**

Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220>
to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:11; N Pos. 12
Seq#:13; N Pos. 16,17,18,19,20,21,22,23,24,25,26,27,28,29,30,31,32,33,34,35
Seq#:13; N Pos. 36,37,38,39,40,41,42,43,44,45,46,47,48,49,50,51,52,53,54,55
Seq#:13; N Pos. 56,57,58,59,60,61,62,63,64,65,66,67,68,69,70,71,72,73,74,75
Seq#:13; N Pos. 76,77,78,79,80,81,82,83,84,85,86,87,88,89,90,91,92
Seq#:16; N Pos. 2
Seq#:18; N Pos. 17
Seq#:19; N Pos. 17

Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:11,12,13,14,15,16,17,18,19

Input Set : **A:\09-754,014.txt**
Output Set: **N:\CRF4\08232004\I754014A.raw**

```
L:468 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0
L:529 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:13 after pos.:0
M:341 Repeated in SeqNo=13
L:546 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:551 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:556 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:14
L:604 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:16 after pos.:0
L:649 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:18 after pos.:0
L:672 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:19 after pos.:0
```